

OM of: US-09-267-199-184 to: SPTREMBL\_12:\* out\_format : pfs

Date: Sep 21, 2000 2:11 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL-frame+ n2p.model -DEV-xlp  
-O/cgn2\_1/USPTO.spool/US09267199/runat\_19092000\_083509\_11226/app\_query.fasta\_1.3044  
-DB-SPTREMBL\_12 -QFWT-fastan -SUFFIX-trans.rspt -GAPOP-12.000  
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000  
-GAPOP-4.500 -GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500  
-GAPOP-6.000 -GAPEXT-7.000 -XGAPOP-10.000 -XGAPEXT-0.500  
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62  
-TRANS-human40.cdi -LIST-45 -DOCLIGN-200 -THR\_SCORE-pct  
-THR\_MAX-100 -THR\_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs  
-NORM-ext -MINLEN-0 -MAXLEN-2000000000  
-USER-US09267199@cgn1\_110 -NCPU-6 -ICPU-3 -LONGLOG -NO\_XLPXY  
-WAIT -THREADS-1

Search information block:

Query: US-09-267-199-184

Database: SPTREMBL\_12:\*

Database sequences: 225878

Database length: 69334122

Search time (sec): 193.520000

score\_list:

Sequence	Strd	Orig	zScore	Escore	Len
sp_plant:024566	+	341.00	662.41	1.4e-29	444
sp_plant:022142	+	339.00	657.31	2.2e-29	520
sp_plant:080428	+	337.00	655.43	3.8e-29	391
sp_bacteria:09X4H2	+	222.00	427.65	1.7e-16	428
sp_bacteria:087006	+	210.00	403.97	3.5e-15	427
sp_bacteria:092FF7	+	210.00	403.97	3.5e-15	427
sp_bacteria:096968	+	193.50	371.30	2.3e-13	432
sp_bacteria:092E00	+	174.50	335.68	2.9e-11	332
sp_archaea:028860	+	116.50	219.44	6.8e-05	419
sp_bacteria:092470	+	115.50	216.22	8.6e-05	498
sp_archaea:09YEK9	+	99.00	184.74	0.0057	427
sp_archaea:028775	+	90.00	167.16	0.0558	416
sp_archaea:09YC47	+	80.00	147.22	0.7010	427
sp_bacteria:092A00	+	74.50	132.66	2.72	711
sp_vertebrate:091287	+	73.50	129.86	3.48	796
sp_bacteria:0926M0	+	70.00	127.17	8.80	445
sp_bacteria:092JC8	+	70.00	125.86	8.69	533
sp_invertebrate:018510	-	70.00	123.02	8.46	788
sp_invertebrate:018511	-	70.00	122.85	8.44	807
sp_archaea:031112	+	69.00	128.76	11.73	272
sp_bacteria:026024	+	69.00	123.89	11.20	533
sp_bacteria:09W10	+	68.50	124.80	12.94	410
sp_bacteria:095659	+	68.50	117.91	12.11	1060
sp_plant:092U07	+	68.00	123.33	14.62	438
sp_vertebrate:p70041	+	67.50	125.86	17.17	270
sp_bacteria:006994	+	67.50	120.55	16.31	561
sp_human:015563	+	66.50	123.09	21.95	301
sp_human:060296	+	66.50	119.88	21.28	469
sp_bacteria:096141	+	66.50	113.97	20.11	1058
sp_bacteria:0921U3	+	66.50	113.97	20.11	1058
sp_bacteria:095585	+	66.50	113.96	20.10	1060
sp_bacteria:095591	+	66.50	113.96	20.10	1060
sp_bacteria:095592	+	66.50	113.96	20.10	1060
sp_bacteria:095593	+	66.50	113.96	20.10	1060
sp_bacteria:095594	+	66.50	113.96	20.10	1060
sp_bacteria:095520	+	66.50	113.96	20.10	1060
sp_bacteria:095638	+	66.50	113.96	20.10	1060
sp_bacteria:095642	+	66.50	113.96	20.10	1060
sp_bacteria:095660	+	66.50	113.96	20.10	1060
sp_bacteria:095641	+	66.50	113.95	20.10	1062

sp\_bacteria:p95658 + 66.50 113.95 20.10 1062 + P95658 rickettsia sp. b2  
sp\_bacteria:052657 + 66.50 109.28 19.22 2021 + 052657 rickettsia conor.  
sp\_bacteria:031371 + 66.00 122.20 24.94 297 + 031371 borrelia garinii. o  
sp\_archaea:058571 + 65.50 121.83 28.47 273 + 058571 methanococcus jannas  
sp\_bacteria:0924U3 + 65.50 120.79 28.19 315 + 0924U3 streptococcus pneumo

seq\_name: sp\_plant:024566

seq\_documentation\_block:

ID 024566 PRELIMINARY; PRT; 444 AA.

AC 024566;

DT 01-JAN-1998 (TREMREL. 05, Created)

DT 01-JAN-1998 (TREMREL. 05, Last sequence update)

DT 01-NOV-1999 (TREMREL. 12, Last annotation update)

DE 3-PROSHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)

DE (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE)

DE (FRAGMENT).

GN EPSP-S.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;

OC Poaceae; Zea.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BMS;

RA LEBRUN M., FREYSSINET M., SAILLAND A., ROLLAND A., FREYSSINET G.;

RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE -

CC O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.

CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS FROM CHORISMATE OF THE

CC AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).

CC -1- SIMILARITY: WITH BACTERIAL, FUNGAL AND PLANT EPSP SYNTHASES.

DR EMBL; X63374; CA44374.1; -

DR MENDEL; 27036; Zeams;419;27036.

DR PROSITE; PS00104; EPSP-SYNTHASE\_1; 1.

DR PROSITE; PS00885; EPSP-SYNTHASE\_2; 1.

DR PFAM; PF00275; EPSP-synthase; 1.

KW Transferase; Aromatic amino acid biosynthesis.

FT NON\_TER 1

SQ SEQUENCE 444 AA; 47282 MW; F36F2E42 CRC32;

alignment\_scores:

Quality: 341.00 Length: 81

Ratio: 4.429 Gaps: 0

Percent Similarity: 95.062 Percent Identity: 80.247

alignment\_block:

US-09-267-199-184 x 024566

Align seg 1/1 to: 024566 from: 1 to: 444

2 GCTTTTGTGAGGTGATGCTTCAAGTGCAGTTACTTCTAGCTGGTGC 51

|||||

247 AlatyVaigluGlyAspAlaSerSerAlaSerTyPheLeuAlaGlyAl 263

|||||

52 AGCAGTAAGTCTGGGACATCATCTGTTAATGCTGTGCCAAGCAGTT 101

|||||

263 alalalThrThrGlyThrValThrValGluGlyCysGlyThrThrSerL 280

|||||

102 TACAGGAGATGATAAATTTGCTGAAGTTCTTGAAGAAGTGGAGCTAAG 151

|||||

280 euGluGlyAspValLysPheAlaGluValLeuGluMetMetGlyAlaLys 296

|||||

152 GTTACATGCTCAGAACAGTGTCCACCGTTACTGGACCGCCACAGATTC 201

|||||

297 ValThrThrThrGlyThrSerValThrValThrGlyProProArgGluPr 313

|||||

202 TCTCTGGTCAAAAGTCTTGCAGGAGCATGATGATCAATATGAC 244

|||||

313 opheGlyArgLysHisLeuLysAlaIleAspValAsnMetAsn 327

|||||

seq\_name: sp\_plant:022142